

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 10, 2002, 08:25:23 ; Search time 25.06 Seconds
(without alignments)
110.452 Million cell updates/sec

Title: US-09-508-054-19

Perfect score: 87

Sequence: 1 YLRVQCRSVESGSGF 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

- SPTREMBL19:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_podent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	95.4	171	4 Q9UNL5	Q9unl5 homo sapien
2	83	95.4	179	4 Q9HBZ1	Q9hbz1 homo sapien
3	83	95.4	202	4 Q14631	Q14631 homo sapien
4	83	95.4	217	4 Q16631	Q16631 homo sapien
5	80	92.0	167	4 P78451	P78451 homo sapien
6	80	92.0	199	4 Q14406	Q14406 homo sapien
7	80	92.0	217	4 Q14407	Q14407 homo sapien
8	77	88.5	212	6 Q07368	Q07368 macaca mula
9	77	88.5	217	6 Q07367	Q07367 macaca mula
10	77	88.5	217	6 Q07369	Q07369 macaca mula
11	51.5	59.2	190	11 Q9JKG0	Q9jkg0 cavia porce
12	51.5	59.2	216	11 Q70615	O70615 spalax leuc
13	51.5	59.2	216	11 Q9R2C3	Q9r2c3 mus musculus
14	51.5	59.2	216	11 Q9JRM4	Q9jkm4 cavia porce
15	47.5	54.6	217	6 Q28957	Q28957 sus scrofa
16	46.5	53.4	28	6 Q9N264	Q9n264 bos taurus

019033	ovis aries	51	6	019033
Q28119	bos taurus	67	6	Q28119
Q28116	bos taurus	73	6	Q28116
Q9TSQ0	ovis aries	120	6	Q9TSQ0
Q9TQW9	bos indicus	192	6	Q9TQW9
Q9CU21	capra hircu	192	6	Q9CU21
Q95205	ovis aries	204	6	Q95205
Q9BEC0	tragulus ja	217	6	Q9BEC0
Q9BEB9	tragulus ja	217	6	Q9BEB9
Q9FME7	arabidopsis	1335	10	Q9FME7
Q35256	mus musculus	227	11	Q35256
Q951R9	macaca fasc	157	6	Q951R9
Q29309	archaeoglob	43	49.4	511
Q9H4Q2	homo sapien	113	4	Q9H4Q2
Q9C9P0	arabidopsis	1286	10	Q9C9P0
Q91741	xenopus lae	1683	13	Q91741
Q9V6A0	drosophila	1929	5	Q9V6A0
Q9SS05	arabidopsis	1036	10	Q9SS05
Q9CKM0	pasteurella	179	16	Q9CKM0
Q9M1L9	arabidopsis	372	10	Q9M1L9
Q62390	mus musculus	554	11	Q62390
Q9V784	magnaporthe	631	3	Q9V784
Q9NF74	drosophila	707	5	Q9NF74
Q9W5C1	drosophila	711	5	Q9W5C1
Q35442	mus musculus	1964	11	Q35442
Q46625	bos taurus	134	6	Q46625
Q9DJL2	cowpox viru	167	12	Q9DJL2
Q9X8T3	streptomyce	197	2	Q9X8T3
P73692	synecocyst	265	16	P73692
Q9S530	chlamydia t	354	2	Q9S530
Q84245	chlamydia t	354	16	Q84245
Q9Z8N6	chlamydia p	360	16	Q9Z8N6
Q9U416	branchiosto	362	5	Q9U416
Q9NCP9	branchiosto	364	5	Q9NCP9
Q9SIT3	arabidopsis	384	10	Q9SIT3
Q13564	homo sapien	534	4	Q13564
Q9Z1A5	rattus norv	534	11	Q9Z1A5
Q9NJA5	babesia bov	1292	5	Q9NJA5
Q90Y12	fugu rubrip	1822	13	Q90Y12
Q75557	homo sapien	2023	4	Q75557
Q9UND7	homo sapien	2023	4	Q9UND7
Q88542	mus musculus	2074	11	Q88542
Q9UHV6	homo sapien	2212	4	Q9UHV6
Q9PVC9	lepisosteus	85	13	Q9PVC9
Q9PVC8	amia calva	89	13	Q9PVC8
Q98SR8	megaloalama	187	13	Q98SR8
Q98SR7	cyprinus ca	188	13	Q98SR7
Q98TT4	megaloalama	188	13	Q98TT4
Q90283	carassius a	188	13	Q90283
Q90W27	carassius a	188	13	Q90W27
Q90W26	carassius a	188	13	Q90W26
Q91386	amia calva	195	13	Q91386
Q91056	hypophthalm	210	13	Q91056
Q90Z01	mylopharyng	210	13	Q90Z01
Q90WY7	catla catla	210	13	Q90WY7
Q90W30	cirrhinus m	210	13	Q90W30
Q63435	rattus norv	229	11	Q63435
Q26765	trypanosoma	527	5	Q26765
Q9CL44	pasteurella	84	16	Q9CL44
Q9RMQ5	acinetobact	127	2	Q9RMQ5
Q9R620	acinetobact	127	2	Q9R620
Q9RMQ3	acinetobact	127	2	Q9RMQ3
Q9RBH6	acinetobact	127	2	Q9RBH6
Q9RBH4	acinetobact	127	2	Q9RBH4
Q91904	acinetobact	127	2	Q91904
Q9F896	acinetobact	127	2	Q9F896
Q9F893	acinetobact	127	2	Q9F893
O42216	necturus ma	158	13	O42216
Q9W798	catla catla	211	13	Q9W798
Q9LU76	arabidopsis	278	10	Q9LU76
Q9PKF1	chlamydia m	354	16	Q9PKF1
Q912U0	pseudomonas	426	11	Q912U0
Q9D8F3	mus musculus	450	11	Q9D8F3

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90 39 44.8 459 5 Q9V5R0
91 39 44.8 493 4 Q96NX2
92 39 44.8 526 3 Q96TU7
93 39 44.8 534 5 Q9V7Q5
94 39 44.8 554 10 Q9S9X4
95 39 44.8 586 4 Q96FC1
96 39 44.8 645 5 Q19780
97 39 44.8 666 5 Q9XU75
98 39 44.8 793 12 Q91BU7
99 39 44.8 841 4 Q96ML9
100 39 44.8 893 5 Q9VLY3
101 39 44.8 1145 2 Q9EZA3
102 39 44.8 1360 5 Q9TYK4
103 38.5 44.3 332 10 Q9FZ14
104 38 43.7 29 10 Q9S8E5
105 38 43.7 31 10 Q9S8E4
106 38 43.7 30 10 Q9S8E3
107 38 43.7 65 6 Q29332
108 38 43.7 70 2 Q87909
109 38 43.7 71 16 Q9JRI9
110 38 43.7 75 2 Q54420
111 38 43.7 75 2 Q54424
112 38 43.7 98 5 Q94423
113 38 43.7 217 13 Q9DGH0
114 38 43.7 240 2 Q47239
115 38 43.7 267 3 Q9HFP0
116 38 43.7 351 11 Q921S5
117 38 43.7 393 5 Q9TVJ1
118 38 43.7 394 10 Q9SU70
119 38 43.7 441 16 Q989K1
120 38 43.7 445 2 Q9KH05
121 38 43.7 524 3 Q9P330
122 38 43.7 535 5 Q9SRU6
123 38 43.7 549 4 Q96SY9
124 38 43.7 561 4 Q9UJE1
125 38 43.7 564 4 Q9UJE2
126 38 43.7 604 4 Q9NXG5
127 38 43.7 914 13 Q12960
128 38 43.7 950 5 Q9VLC3
129 38 43.7 1052 5 Q9VS50
130 38 43.7 1265 5 Q9U8F6
131 37.5 43.1 165 13 Q97487
132 37.5 43.1 202 3 Q01615
133 37.5 43.1 210 13 Q91160
134 37.5 43.1 642 3 Q97239
135 37.5 43.1 911 3 Q96VJ4
136 37.5 43.1 1044 3 Q94173
137 37.5 43.1 1079 3 Q96V11
138 37.5 43.1 1088 3 Q07242
139 37.5 43.1 1092 3 Q9UVY2
140 37.5 43.1 6781 12 Q91AV2
141 37 42.5 57 5 Q9Y0B0
142 37 42.5 81 5 Q9Y0A9
143 37 42.5 82 5 Q9U6U0
144 37 42.5 86 16 Q98AH9
145 37 42.5 95 5 Q76327
146 37 42.5 109 3 Q9URD6
147 37 42.5 127 2 Q9RMO4
148 37 42.5 127 2 Q9RBC9
149 37 42.5 127 2 Q9F894
150 37 42.5 216 13 Q98T88
```

ALIGNMENTS

```
RESULT 1
Q9UNL5
ID Q9UNL5 PRELIMINARY; PRT; 171 AA.
AC Q9UNL5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-DEC-2001 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
```

```
DE GROWTH HORMONE SPLICE VARIANT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=PIUITARY;
RA Song H., Peng Y., Dai M., Huang Q., Mao Y., Zhang Q., Mao M., Fu G.,
RT Luo M., Chen J., Hu R.;
RT "Human growth hormone variant splicing gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110644; AAD48584.1; -.
DR HSSP; P01241; IAXI.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 2.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 171 AA; 19801 MW; 9FA9013991FA9F28 CRC64;
```

Query Match 95.4%; Score 83; DB 4; Length 171;
Best Local Similarity 93.8%; Pred. No. 2.8e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 YLRIVQCRSVEGSCGF 16
Db 156 FLRIVQCRSVEGSCGF 171
:|||||
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RESULT 2
Q9HBZ1 PRELIMINARY; PRT; 179 AA.
ID Q9HBZ1
AC Q9HBZ1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GROWTH HORMONE VARIANT.
GN GHV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=PIUITARY;
RA Gu J., Huang Q., Li N., Xu S., Han Z., Fu G., Chen Z.;
RT "A novel gene expressed in human pituitary.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF185611; AAG09699.1; -.
DR HSSP; P01241; IAXI.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 2.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 179 AA; 20561 MW; 0E875A91BE0B9B7E CRC64;
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Query Match 95.4%; Score 83; DB 4; Length 179;
Best Local Similarity 93.8%; Pred. No. 2.9e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 YLRIVQCRSVEGSCGF 16
Db 164 FLRIVQCRSVEGSCGF 179
:|||||
```

```
RESULT 3
O14643 PRELIMINARY; PRT; 202 AA.
ID O14643
AC O14643;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
```

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PLACENTAL GROWTH HORMONE 20KDA ISOFORM PRECURSOR.
 GN HGH-V.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FULL-TERM PLACENTA;
 RX MEDLINE=98373737; PubMed=9709963;
 RA Boguszewski C.L., Svensson P.A., Jansson T., Clark R.,
 RA Carlsson L.M.S., Carlsson B.;
 RT "Cloning of two novel growth hormone transcripts expressed in human
 placenta.";
 RL J. Clin. Endocrinol. Metab. 83:2878-2885(1998).
 DR EMBL: AF006060; AAB1828.1; -;
 DR HSSP: P01241; 1A22.
 DR InterPro: IPR001400; SOMATOTROPIN.
 DR Pfam: PF00103; hormone; 2.
 DR PRINTS: PR00836; SOMATOTROPIN.
 DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
 DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
 KW SIGNAL.
 FT SIGNAL. 1 26 POTENTIAL.
 SQ SEQUENCE 202 AA; 23128 MW; 38B64D011A9197C6 CRC64;

 Query Match 95.4%; Score 83; DB 4; Length 202;
 Best Local Similarity 93.8%; Pred. No. 3.2e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YLRIVQCRSVEGSCGF 16
 DB 187 FLRIVQCRSVEGSCGF 202

 RESULT 4
 Q16631
 ID Q16631 PRELIMINARY; PRT; 217 AA.
 AC Q16631; Q14405;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GROWTH HORMONE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=82014939; PubMed=6269091;
 RX Denoto F.M., Moore D.D., Goodman H.M.;
 RA "Human growth hormone DNA sequence and mRNA structure: possible
 alternative splicing.";
 RT Nucleic Acids Res. 9:3719-3730(1981).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84057143; PubMed=6357679;
 RA Adelman J.P., Hayflick J.S., Vasser M., Seeburg P.H.;
 RT "In vitro deletional mutagenesis for bacterial production of the
 20,000-dalton form of human pituitary growth hormone.";
 RL DNA 2:183-193(1983).
 DR EMBL: V00520; CAA23779.1; -;
 DR HSSP: P01241; 1HGU.
 DR InterPro: IPR001400; SOMATOTROPIN.
 DR Pfam: PF00103; hormone; 1.
 DR PRINTS: PR00836; SOMATOTROPIN.
 DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
 DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
 SQ SEQUENCE 217 AA; 24803 MW; CCC4D81150D908AC CRC64;

Query Match 95.4%; Score 83; DB 4; Length 217;
 Best Local Similarity 93.8%; Pred. No. 3.5e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YLRIVQCRSVEGSCGF 16
 DB 202 FLRIVQCRSVEGSCGF 217

 RESULT 5
 P78451
 ID P78451 PRELIMINARY; PRT; 167 AA.
 AC P78451;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SOMATOMAMMOTROPIN (CHORIONIC SOMATOMAMMOTROPIN) (HCS) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=78071761; PubMed=593368;
 RA Shine J., Seeburg P.H., Martial J.A., Baxter J.D., Goodman H.M.;
 RT "Construction and analysis of recombinant DNA for human chorionic
 somatomammotropin.";
 RL Nature 270:494-499(1977).
 RN [2]
 RP SEQUENCE OF 110-167 FROM N.A.
 RX MEDLINE=78160787; PubMed=611657;
 RA Seeburg P.H., Shine J., Martial J.A., Ullrich A., Goodman H.M.,
 RA Baxter J.D.;
 RT "Nucleotide sequence of a human gene coding for a polypeptide
 hormone.";
 RL Trans. Assoc. Am. Physicians 90:109-116(1977).
 DR EMBL: V00593; CAA23840.1; -;
 DR EMBL: M25118; AAA35721.1; -;
 DR HSSP: P01241; 1A22.
 DR InterPro: IPR001400; SOMATOTROPIN.
 DR Pfam: PF00103; hormone; 1.
 DR PRINTS: PR00836; SOMATOTROPIN.
 DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
 DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
 KW Chorion.
 FT NON_TER.
 SQ SEQUENCE 167 AA; 19586 MW; 6EC7829D3938E976 CRC64;

 Query Match 92.0%; Score 80; DB 4; Length 167;
 Best Local Similarity 87.5%; Pred. No. 9.4e-07;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YLRIVQCRSVEGSCGF 16
 DB 152 FLRMVQCRSVEGSCGF 167

 RESULT 6
 Q14406
 ID Q14406 PRELIMINARY; PRT; 199 AA.
 AC Q14406;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CHORIONIC SOMATOMAMMOTROPIN CS-5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89307277; PubMed=2744760;

RA Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinias R.E.,
 RA Seeburg P.H.;
 RT "The human growth hormone locus: nucleotide sequence, biology, and
 RT evolution.";
 RL Genomics 4:479-497(1989).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE-91102558; PubMed-1980158;
 RA Vnencak-Jones C.L., Phillips J.A. III.;
 RT "Hot spots for growth hormone gene deletions in homologous regions
 RT outside of Alu repeats.";
 RL Science 250:1745-1748(1990).
 DR EMBL: J03071; AAA52550.1; -;
 DR HSSP: P01241; 1A22.
 DR InterPro: IPR001400; SOMATOTROPIN.
 DR Pfam: PF00103; hormone; 2.
 DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
 SQ SEQUENCE 199 AA; 22649 MW; 119656E87AFD55C3 CRC64;

Query Match 92.0%; Score 80; DB 4; Length 199;
 Best Local Similarity 87.5%; Pred. No. 1.1e-06;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLRIVQCRSVEGSCGF 16
 :||:|||||
 DB 184 FLRMVQCRSVEGSCGF 199

RESULT 7
 ID Q14407 PRELIMINARY; PRT; 217 AA.
 AC Q14407;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE CHORIONIC SOMATOMAMOTROPIN CS-2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89307277; PubMed-2744760;
 RA Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinias R.E.,
 RA Seeburg P.H.;
 RT "The human growth hormone locus: nucleotide sequence, biology, and
 RT evolution.";
 RL Genomics 4:479-497(1989).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE-91102558; PubMed-1980158;
 RA Vnencak-Jones C.L., Phillips J.A. III.;
 RT "Hot spots for growth hormone gene deletions in homologous regions
 RT outside of Alu repeats.";
 RL Science 250:1745-1748(1990).
 DR EMBL: J03071; AAA52553.1; -;
 DR HSSP: P01241; 1A22.
 DR InterPro: IPR001400; SOMATOTROPIN.
 DR Pfam: PF00103; hormone; 1.
 DR PRINTS: PR00836; SOMATOTROPIN.
 DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
 DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
 SQ SEQUENCE 217 AA; 24994 MW; 39FAACDDB6B2E951 CRC64;

Query Match 92.0%; Score 80; DB 4; Length 217;
 Best Local Similarity 87.5%; Pred. No. 1.2e-06;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLRIVQCRSVEGSCGF 16
 :||:|||||
 DB 202 FLRMVQCRSVEGSCGF 217

RESULT 8
 Q07368
 ID Q07368 PRELIMINARY; PRT; 212 AA.
 AC Q07368;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE SOMATOTROPIN 2 PRECURSOR (GROWTH HORMONE 2) (FRAGMENT).
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RX MEDLINE-94008724; PubMed-8404617;
 RA Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
 RT "Cloning of four growth hormone/chorionic somatomotropin-related
 RT complementary deoxyribonucleic acids differentially expressed during
 RT pregnancy in the rhesus monkey placenta.";
 RL Endocrinology 133:1744-1752(1993).
 CC - FUNCTION: GROWTH HORMONE PLAYS AN IMPORTANT ROLE IN GROWTH
 CC CONTROL.
 CC - SUBCELLULAR LOCATION: SECRETED.
 CC - SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
 DR EMBL: L16553; AAA18840.1; -;
 DR HSSP: P01241; 1AXI.
 DR InterPro: IPR001400; SOMATOTROPIN.
 DR Pfam: PF00103; hormone; 1.
 DR PRINTS: PR00836; SOMATOTROPIN.
 DR PROSITE: PS00338; SOMATOTROPIN_2; UNKNOWN_1.
 KW Pituitary; Hormone; Signal.
 FT NON_TER 1
 FT SIGNAL <1 ?
 FT CHAIN ? 212 SOMATOTROPIN 2.
 FT DISULFID 74 186 BY SIMILARITY.
 FT DISULFID 203 210 BY SIMILARITY.
 SQ SEQUENCE 212 AA; 24525 MW; 27BC91106256E6F5 CRC64;

Query Match 88.5%; Score 77; DB 6; Length 212;
 Best Local Similarity 81.2%; Pred. No. 4.1e-06;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLRIVQCRSVEGSCGF 16
 :||:||||:|||||
 DB 197 FLRMVQCRSVEGSCGF 212

RESULT 9
 Q07367
 ID Q07367 PRELIMINARY; PRT; 217 AA.
 AC Q07367;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE SOMATOTROPIN 1 PRECURSOR (GROWTH HORMONE 1).
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RX MEDLINE-94008724; PubMed-8404617;
 RA Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
 RT "Cloning of four growth hormone/chorionic somatomotropin-related
 RT complementary deoxyribonucleic acids differentially expressed during
 RT pregnancy in the rhesus monkey placenta.";

RL Endocrinology 133:1744-1752(1993).
CC -!- FUNCTION: GROWTH HORMONE PLAYS AN IMPORTANT ROLE IN GROWTH
CC CONTROL.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
DR EMBL; L16552; AA18839.1; -.
DR HSSP; P01241; IAXI.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
KW Pituitary; Hormone; Signal.
FT SIGNAL 1 ?
FT CHAIN ? 217 SOMATOTROPIN 1.
FT DISULFID 79 191 BY SIMILARITY.
FT DISULFID 208 215 BY SIMILARITY.
SQ SEQUENCE 217 AA; 24942 MW; F5AA8915131F2BC CRC64;

Query Match 88.5%; Score 77; DB 6; Length 217;
Best Local Similarity 81.2%; Pred. NO. 4.2e-06;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLRIVQCRSVEGSCGF 16
:||||:|||||
Db 202 FLRMVQCRTEGSCGF 217

RESULT 10
Q07369 PRELIMINARY; PRT; 217 AA.
AC Q07369;

DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SOMATOTROPIN 3 PRECURSOR (GROWTH HORMONE 3).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA MEDLINE=94008724; PubMed=8404617;
RA Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
RT "Cloning of four growth hormone/chorionic somatomammotropin-related
RT complementary deoxyribonucleic acids differentially expressed during
RT pregnancy in the rhesus monkey placenta.";
RL Endocrinology 133:1744-1752(1993).
CC -!- FUNCTION: GROWTH HORMONE PLAYS AN IMPORTANT ROLE IN GROWTH
CC CONTROL.

CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
DR EMBL; L16554; AA18841.1; -.
DR HSSP; P01241; IAXI.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
KW Pituitary; Hormone; Signal.
FT SIGNAL 1 ?
FT CHAIN ? 217 SOMATOTROPIN 3.
FT DISULFID 79 191 BY SIMILARITY.
FT DISULFID 208 215 BY SIMILARITY.
SQ SEQUENCE 217 AA; 24874 MW; F1EB6AFDBA1B185 CRC64;

Query Match 88.5%; Score 77; DB 6; Length 217;
Best Local Similarity 81.2%; Pred. NO. 4.2e-06;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLRIVQCRSVEGSCGF 16
:||||:|||||
Db 202 FLRMVQCRTEGSCGF 217

RESULT 11

ID Q9JUG0 PRELIMINARY; PRT; 190 AA.
AC Q9JUG0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GROWTH HORMONE (FRAGMENT).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=20231762; PubMed=10767558;
RA Adkins R.M., Vandeberg J., Li W.H.;
RT "Molecular evolution of growth hormone and receptor in the guinea-pig,
RT a mammal unresponsive to growth hormone.";
RL Gene 246:357-363(2000).
DR EMBL; AF238493; AAF67172.1; -.
DR HSSP; P01246; 1BST.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 190 AA; 21962 MW; 6A0394FC5E707BE8 CRC64;

Query Match 59.2%; Score 51.5; DB 11; Length 190;
Best Local Similarity 58.8%; Pred. NO. 0.15;
Matches 10; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 YLRIVQCRS-VEGSCGF 16
:||||:|||||
Db 174 YLRVMKCRFEVSSCAF 190

RESULT 12
O70615 PRELIMINARY; PRT; 216 AA.
ID O70615;

DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GROWTH HORMONE PRECURSOR.
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
OC Spalax.
OX NCBI_TaxID=30637;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99124645; PubMed=9924177;
RA Lioupis A., Nevo E., Wallis M.;
RT "Cloning and characterisation of the gene encoding mole rat (Spalax
RT ehrenbergi) growth hormone.";
RL J. Mol. Endocrinol. 22:29-36(1999).
DR EMBL; AJ005819; CAA06716.1; -.
DR HSSP; P01246; 1BST.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.

FT CHAIN 27 216 GROWTH HORMONE.
SQ SEQUENCE 216 AA; 24627 MW; EEAB8A523BA0ADFE CRC64;

Query Match 59.2%; Score 51.5; DB 11; Length 216;
Best Local Similarity 58.8%; Pred. No. 0.17;
Matches 10; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 YLRIVOCRS-VEGSCGF 16
|||::||| || || |

Db 200 YLRVMKRRFVSSCAF 216

RESULT 13
Q9R2C3 PRELIMINARY; PRT; 216 AA.

AC Q9R2C3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE GROWTH HORMONE.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Nguyen T.N.K., Liebhaber S.A.;
RT "Mouse Growth Hormone Locus: Nucleotide Sequence and Phylogenetic Analyses";

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; U34362; AAC99988.1; -.

DR HSSP; P01246; 1BST.

DR InterPro; IPR001400; SOMATOTROPIN.

DR Pfam; PF00103; hormone; 1.

DR PRINTS; PR00836; SOMATOTROPIN.

DR PROSITE; PS00266; SOMATOTROPIN_1; 1.

DR PROSITE; PS00338; SOMATOTROPIN_2; 1.

SQ SEQUENCE 216 AA; 24682 MW; FC2A05DA02536B18 CRC64;

Query Match 59.2%; Score 51.5; DB 11; Length 216;
Best Local Similarity 58.8%; Pred. No. 0.17;
Matches 10; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 YLRIVOCRS-VEGSCGF 16
|||::||| || || |

Db 200 YLRVMKRRFVSSCAF 216

RESULT 14
Q9JKM4 PRELIMINARY; PRT; 216 AA.

AC Q9JKM4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GROWTH HORMONE PRECURSOR.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RA Odorico D.M., Fuller P.J., Herington A.C.;

RT "Cloning and sequence of guinea pig growth hormone (GH).";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF233853; AAF36409.1; -.

DR HSSP; P01246; 1BST.

DR InterPro; IPR001400; SOMATOTROPIN.

DR Pfam; PF00103; hormone; 1.

DR PRINTS; PR00836; SOMATOTROPIN.

DR PROSITE; PS00266; SOMATOTROPIN_1; 1.

DR PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
KW Signal. 1 26 POTENTIAL.
FT CHAIN 27 216 GROWTH HORMONE.
SQ SEQUENCE 216 AA; 24822 MW; 45996BE119B08DD3 CRC64;

Query Match 59.2%; Score 51.5; DB 11; Length 216;
Best Local Similarity 58.8%; Pred. No. 0.17;
Matches 10; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 YLRIVOCRS-VEGSCGF 16
|||::||| || || |

Db 200 YLRVMKRRFVSSCAF 216

RESULT 15

Q28957

ID Q28957 PRELIMINARY; PRT; 217 AA.

AC Q28957;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GROWTH HORMONE.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PITUITARY;

RA Qi S.-z., Wang X.-z., Zhou S.-w., Jia F., Wang H.-y., Xia, Li, Li J.;

RT "cDNA sequence og the porcine growth hormone.";

RL Chin. J. Biotechnol. 5:35-39(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=PITUITARY;

RA Xu L.;

RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; U19787; AAA73477.1; -.

DR HSSP; P01246; 1BST.

DR InterPro; IPR001400; SOMATOTROPIN.

DR Pfam; PF00103; hormone; 1.

DR PRINTS; PR00836; SOMATOTROPIN.

DR PROSITE; PS00266; SOMATOTROPIN_1; 1.

SQ SEQUENCE 217 AA; 24470 MW; F708195D8A678831 CRC64;

Query Match 54.6%; Score 47.5; DB 6; Length 217;
Best Local Similarity 58.8%; Pred. No. 0.92;
Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 YLRIVOCRS-VEGSCGF 16
|||::||| || || |

Db 201 YLRAMKRRFVSSCAF 217

RESULT 16

Q9N264

ID Q9N264 PRELIMINARY; PRT; 28 AA.

AC Q9N264;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GROWTH HORMONE (FRAGMENT).

GN BGH.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

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RA Lagziel A., Soller M.;
RT "DNA sequence of SSCP haplotypes at the bovine growth hormone (bgh)
RL gene."
RL Anim. Genet. 0:0-0(1999).
DR EMBL: AF117350; AAF28806.1; -.
DR HSP: P01246; 1BST.
DR InterPro: IPR001400; SOMATOTROPIN.
DR Pfam: PF00103; hormone; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 28 AA; 3397 MW; 39B00CE59B01B926 CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 28;
Best Local Similarity 52.9%; Pred. No. 0.18;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRVQCRSV-EGSCGF 16
DB 12 YLRVMKRRFGEASCAF 28

RESULT 17
OL0933 PRELIMINARY; PRT; 51 AA.
AC O19033;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GROWTH HORMONE (FRAGMENT).
GN GH.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ROMANOV;
RA Ofir R., Gootwine E.;
RT "Sequence analysis of the GH1, GH2-N and GH2-Z copies of the ovine
RT growth hormone gene."
RL Mamm. Genome 0:0-0(1997).
DR EMBL: AF002117; AAB64117.1; -.
DR HSP: P01246; 1BST.
DR InterPro: IPR001400; SOMATOTROPIN.
DR Pfam: PF00103; hormone; 1.
DR PRINTS: PR00836; SOMATOTROPIN.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 51 AA; 6083 MW; 7358BBC165696B23 CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 51;
Best Local Similarity 52.9%; Pred. No. 0.33;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRVQCRSV-EGSCGF 16
DB 35 YLRVMKRRFGEASCAF 51

RESULT 18
Q28119 PRELIMINARY; PRT; 67 AA.
AC Q28119;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GROWTH HORMONE (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=87204193; PubMed=3472230;
RA Hampson R.K., Rottman F.M.;
RT "Alternative processing of bovine growth hormone mRNA: Nonsplicing of
RT the final intron predicts a high molecular weight variant of bovine
RT growth hormone."
RL Proc. Natl. Acad. Sci. U.S.A. 84:2673-2677(1987).
DR EMBL: M16253; AAA30547.1; -.
DR HSP: P01246; 1BST.
DR InterPro: IPR001400; SOMATOTROPIN.
DR Pfam: PF00103; hormone; 1.
DR PRINTS: PR00836; SOMATOTROPIN.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 67 AA; 7793 MW; 757AA5D81CDE2CC8 CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 67;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRVQCRSV-EGSCGF 16
DB 51 YLRVMKRRFGEASCAF 67

RESULT 19
Q28116 PRELIMINARY; PRT; 73 AA.
AC Q28116;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GROWTH HORMONE C VARIANT (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Chikuni K., Nagatsuma T., Tabata T., Monma M., Saito M., Ozawa S.,
RA Ozutsumi K.;
RT "Genetic variants of the growth hormone gene in Japanese cattle."
RL Anim. Sci. Technol. 65:340-346(1994).
DR EMBL: D30713; BAA06379.1; -.
DR HSP: P01246; 1BST.
DR InterPro: IPR001400; SOMATOTROPIN.
DR Pfam: PF00103; hormone; 1.
DR PRINTS: PR00836; SOMATOTROPIN.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FT NON_TER 1
FT VARIANT 9
FT VARIANT 54
SQ SEQUENCE 73 AA; 8468 MW; 95D6485BEECD3BC CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 73;
Best Local Similarity 52.9%; Pred. No. 0.48;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

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QY 1 YLRVQCRSV-EGSCGF 16
    |||::||| | | |
Db 57 YLRVMKRRFGEASCAF 73

RESULT 20
Q9TSG0 PRELIMINARY; PRT; 120 AA.
AC Q9TSG0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GROWTH HORMONE (FRAGMENT).
GN GH.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ROMANOV;
RA Ofir R., Gootwine E.;
RT "Sequence analysis of the GH1, GH2-N and GH2-Z copies of the ovine
    growth hormone gene.";
RL Mamm. Genome 0:0-0(1997).
DR EMBL; AF002120; AAB64120.1; -.
DR HSP; P01246; IBST.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 120 AA; 13972 MW; 2622C4FA10294C52 CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 120;
Best Local Similarity 52.9%; Pred. No. 0.78;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRVQCRSV-EGSCGF 16
    |||::||| | | |
Db 104 YLRVMKRRFGEASCAF 120

RESULT 21
Q9TQW9 PRELIMINARY; PRT; 192 AA.
AC Q9TQW9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GROWTH HORMONE.
OS Bos indicus (Zebu), and
    Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9915; 89462;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDIAN;
RA Mukhopadhyay U.K., Sahni G.;
RT "Indian zebu cattle growth hormone cDNA.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177289; AAF03132.1; -.
DR EMBL; AF177288; AAF03131.1; -.
DR HSP; P01246; IBST.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
SQ SEQUENCE 192 AA; 21977 MW; ASA6977B607F31BA CRC64;
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DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 192 AA; 21947 MW; 0C7B5EAF606B3ECC CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 192;
Best Local Similarity 52.9%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRVQCRSV-EGSCGF 16
    |||::||| | | |
Db 176 YLRVMKRRFGEASCAF 192

RESULT 22
Q9TU21 PRELIMINARY; PRT; 192 AA.
ID Q9TU21;
AC Q9TU21;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GROWTH HORMONE.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDIAN BEETAL;
RA Mukhopadhyay U.K., Sahni G.;
RT "Indian goat growth hormone cDNA.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177287; AAF03130.1; -.
DR HSP; P01246; IBST.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 192 AA; 21977 MW; ASA6977B607F31BA CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 192;
Best Local Similarity 52.9%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRVQCRSV-EGSCGF 16
    |||::||| | | |
Db 176 YLRVMKRRFGEASCAF 192

RESULT 23
Q95205 PRELIMINARY; PRT; 204 AA.
ID Q95205;
AC Q95205;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLACENTAL GROWTH HORMONE (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=97050633; PubMed=8895361;
RA Lacroix M.C., Devinoy E., Servely J.L., Puissant C., Kann G.;
RT "Expression of the growth hormone gene in ovine placenta: detection
    and cellular localization of the protein.";
RL Endocrinology 137:4886-4892(1996).
DR EMBL; U49063; AAC48679.1; -;
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DR HSP; P01246; 1BST.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 204 AA; 23462 MW; EBBB9451892635C6 CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 204;
Best Local Similarity 52.9%; Pred. No. 1.3;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRIVQCRSV-EGSCGF 16
|||::||| | || |
DB 188 YLRVVKRRFGEASCAF 204

RESULT 24
Q9BEC0 PRELIMINARY; PRT; 217 AA.
AC Q9BEC0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GROWTH HORMONE-1 PROTEIN PRECURSOR.
GN GH-1.
OS Tragulus javanicus (Lesser Malay chevrotain).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OC Tragulidae; Tragulus.
OX NCBI_TaxID=9849;
RN [1]
RP SEQUENCE FROM N.A.
SQ SEQUENCE 204 AA; 23462 MW; EBBB9451892635C6 CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 204;
Best Local Similarity 52.9%; Pred. No. 1.3;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRIVQCRSV-EGSCGF 16
|||::||| | || |
DB 188 YLRVVKRRFGEASCAF 204

RESULT 24
Q9BEC0 PRELIMINARY; PRT; 217 AA.
AC Q9BEC0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GROWTH HORMONE-1 PROTEIN PRECURSOR.
GN GH-1.
OS Tragulus javanicus (Lesser Malay chevrotain).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OC Tragulidae; Tragulus.
OX NCBI_TaxID=9849;
RN [1]
RP SEQUENCE FROM N.A.
SQ SEQUENCE 204 AA; 23462 MW; EBBB9451892635C6 CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 217;
Best Local Similarity 52.9%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRIVQCRSV-EGSCGF 16
|||::||| | || |
DB 201 YLRVVKRRFGEASCAF 217

RESULT 25
Q9BEB9 PRELIMINARY; PRT; 217 AA.
AC Q9BEB9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GROWTH HORMONE-2 PROTEIN PRECURSOR.
GN GH-2.

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OS Tragulus javanicus (Lesser Malay chevrotain).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OC Tragulidae; Tragulus.
OX NCBI_TaxID=9849;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=21434966; PubMed=11551118;
RA Wallis O.C., Wallis M.;
RT "Molecular evolution of growth hormone (GH) in Cetartiodactyla: Cloning and characterization of the gene encoding GH from a primitive ruminant, the chevrotain (Tragulus javanicus).";
RL Gen. Comp. Endocrinol. 123:62-72(2001).
DR EMBL; AJ309714; CAC29337.1; -.
DR HSP; P01246; 1BST.
DR InterPro; IPR001400; SOMATOTROPIN.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Signal.
FT SIGNAL. 1 27 POTENTIAL.
FT CHAIN 28 217 GROWTH HORMONE.
SQ SEQUENCE 217 AA; 24635 MW; 3B89CCFA72EA7BDE CRC64;

Query Match 53.4%; Score 46.5; DB 6; Length 217;
Best Local Similarity 52.9%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 YLRIVQCRSV-EGSCGF 16
|||::||| | || |
DB 201 YLRVVKRRFGEASCAF 217

RESULT 26
Q9FME7 PRELIMINARY; PRT; 1335 AA.
AC Q9FME7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KINESIN-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98162728; PubMed=9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";
RL DNA Res. 4:401-414(1997).
DR EMBL; AB008269; BAB10642.1; -.
DR HSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 1335 AA; 149684 MW; 2B9AEBEBD9DED4A2 CRC64;

Query Match 52.9%; Score 46; DB 10; Length 1335;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      6 QCRSVGSCG 15
      ||| : ||||
Db     1074 QCRATKSCG 1083

RESULT 27
O35256
ID      O35256      PRELIMINARY;      PRT;      227 AA.
AC      O35256;
DT      01-JAN-1998 (TrEMBLrel. 05, Created)
DT      01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE      PROLACTIN-LIKE PROTEIN A PRECURSOR.
GN      PLPA OR PLP-A.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Muller H., Ishimura R., Orwig K.E., Liu B., Soares M.J.;
RL      Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J;
RX      MEDLINE=98049410; PubMed=9389542;
RA      Lin J., Poole J., Linzer D.I.;
RT      "Three new members of the mouse prolactin/growth hormone family are
RT      homologous to proteins expressed in the rat.";
RL      Endocrinology 138:5541-5549(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J;
RA      Lin J., Poole J., Linzer D.I.;
RL      Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF015562; AAB68824.1; -.
DR      EMBL; AF011383; AAB92399.1; -.
DR      HSSP; Q28632; 1AN3.
DR      MGD; MGI:1206587; Plpa.
DR      InterPro: IPR001400; SOMATOTROPIN.
DR      Pfam; PF00103; hormone; 1.
DR      PRINTS; PR00836; SOMATOTROPIN.
DR      PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR      PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
KW      Signal.
FT      SIGNAL.
FT      CHAIN.
SQ      SEQUENCE      227 AA; 26336 MW; 585B2731DCED57B6 CRC64;

      Query Match      50.6%; Score 44; DB 11; Length 227;
      Best Local Similarity 35.7%; Pred. No. 4.2;
      Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1 YLRIVQCRSVGSCG 14
      ||::||| : :|
Db     214 YLKLLKRLIQSNC 227

RESULT 28
Q95LR9
ID      Q95LR9      PRELIMINARY;      PRT;      157 AA.
AC      Q95LR9;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      HYPOTHETICAL 17.5 KDA PROTEIN.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC      Cercopitheciinae; Macaca.
OX      NCBI_TaxID=9541;

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RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=TESTIS;
RA      Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA      Terao K., Sugano S.;
RT      "Isolation of novel full-length cDNA clones from macaque testis cDNA
RT      libraries.";
RL      Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AB071123; BAB64517.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE      157 AA; 17526 MW; 4366390E7064FF9F CRC64;

      Query Match      49.4%; Score 43; DB 6; Length 157;
      Best Local Similarity 61.5%; Pred. No. 4.4;
      Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 LRIVQCRSVGSCG 14
      ||||| : |||
Db     121 LRIVDKRSEGFC 133

RESULT 29
O29309
ID      O29309      PRELIMINARY;      PRT;      511 AA.
AC      O29309;
DT      01-JAN-1998 (TrEMBLrel. 05, Created)
DT      01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      GLUTAMATE SYNTHASE (GLTB).
GN      AF0953.
OS      Archaeoglobus fulgidus.
OC      Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OX      Archaeoglobus.
OX      NCBI_TaxID=2234;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX      MEDLINE=98049343; PubMed=9389475;
RA      Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA      Richardson D.L., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA      Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA      Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA      Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA      Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA      Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA      Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA      Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA      Venter J.C.;
RT      "The complete genome sequence of the hyperthermophilic, sulphate-
RT      reducing archaeon Archaeoglobus fulgidus.";
RL      Nature 390:364-370(1997).
DR      EMBL; AE001038; AAB90287.1; -.
DR      HSSP; P55907; 1XER.
DR      TIGR; AF0953; -.
DR      InterPro: IPR001450; 4Fe4S_ferredoxin.
DR      InterPro: IPR003009; FMN_enzyme.
DR      InterPro: IPR002932; Glu_synthase.
DR      Pfam; PF00037; fer4; 2.
DR      Pfam; PF01645; Glu_synthase; 1.
DR      PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW      Hypothetical protein; Iron-sulfur; Complete proteome.
SQ      SEQUENCE      511 AA; 56203 MW; 0FA661F793D6983F CRC64;

      Query Match      49.4%; Score 43; DB 17; Length 511;
      Best Local Similarity 50.0%; Pred. No. 14;
      Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3 RIVQCRSVGSCGF 16
      |::||| | |||
Db     23 RCIRCVQCRCGF 36

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DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TyRkC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase
SQ SEQUENCE 1286 AA; 143488 MW; DE17E1118FDB7BCA CRC64;

Query Match 48.3%; Score 42; DB 10; Length 1286;
Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 QCRSVGSGCGF 16
DB 195 ECLSSHGSGCF 205

RESULT 32
Q91741 ID Q91741 PRELIMINARY; PRT; 1683 AA.
AC Q91741;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FOURTH COMPONENT OF COMPLEMENT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96186527; PubMed=8606056;
RA Mo R., Kato Y., Nonaka M., Nakayama K., Takahashi M.;
RT "Fourth component of Xenopus laevis complement: cDNA cloning and
RT linkage analysis of the frog MHC.";
RL Immunogenetics 43:360-369(1996).
DR EMBL: D78003; BAA11188.1; -.
DR HSSP: P01024; 1C3D.
DR InterPro: IPR002890; A2M_N.
DR InterPro: IPR001599; Alpha_2_macroglobl.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR001840; Anaphylatoxin.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF00207; A2M; 1.
DR Pfam: PF01835; A2M_N; 1.
DR Pfam: PF01821; ANATO; 1.
DR Pfam: PF01759; NTR; 1.
DR PRINTS: PR00004; ANAPHYLATOXN.
DR ProDom: PD003264; Anaphylatoxin.
DR SMART: SM00104; ANATO; 1.
DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; UNKNOWN_1.
DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
DR MHC.
SQ SEQUENCE 1683 AA; 189707 MW; 0F055063F4A58D96 CRC64;

Query Match 48.3%; Score 42; DB 13; Length 1683;
Best Local Similarity 53.3%; Pred. No. 69;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YLRIVQCRSVGSGC 15
DB 1039 YLRILQFKKADGSYG 1053

RESULT 33

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RESULT 30

Q9H402

ID Q9H402

AC Q9H402 PRELIMINARY; PRT; 113 AA.

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE EP2C.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Frohlich O., Po C., Young L.G.;

RT "Genomic organization of the human epididymal EP2 gene and its

RT relationship to defensin genes.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY005129; AAG21880.1; -.

DR InterPro: IPR001230; Prenyltn.

DR PROSITE: PS00294; PRENYLIATION; UNKNOWN_1.

SQ SEQUENCE 113 AA; 12686 MW; F962A417664352A3 CRC64;

Query Match

Best Local Similarity 48.3%; Score 42; DB 4; Length 113;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LRIVQCRSVGSGC 14

DB 77 LKVDCCRSEGFC 89

RESULT 31

Q9C9P0

ID Q9C9P0

AC Q9C9P0 PRELIMINARY; PRT; 1286 AA.

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

DE PROTEIN KINASE, PUTATIVE.

GN F4N21.1.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RX MEDLINE=21016719; PubMed=11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.B., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,

RA Millitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pali G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Saizerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis

RT thaliana.";

RL Nature 408:816-820(2000).

DR EMBL: AC013288; AAG60067.1; -.

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Q9V6A0
ID Q9V6A0 PRELIMINARY; PRT: 1929 AA.
AC Q9V6A0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE CG13162 PROTEIN.
GN CG13162
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Efankoch C., Baldwin D.,
RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flosser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Housh K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003822; AAF58528.1; -.
DR FlyBase; FBgn0033718; CG13162.
SQ SEQUENCE 1929 AA; 219961 MW; A409187CC6A6CA66 CRC64;

Query Match 48.3%; Score 42; DB 5; Length 1929;
Best Local Similarity 63.6%; Pred. NO. 79;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 IVQCRSVEGSC 14
: | | | | |
Db 347 LAYCNSVEGSC 357

RESULT 34
Q9SS05
ID Q9SS05 PRELIMINARY; PRT: 1036 AA.
AC Q9SS05;

QY 1 YLRIVQCRSVEG-SCGF 16
| | | | | | | |
Db 863 YLKVVNCESLERLDCSF 879

RESULT 35
Q9CKM0 PRELIMINARY; PRT: 179 AA.
AC Q9CKM0;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NAPP.
GN NAPP OR PM1592.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006197; AAK03676.1; -.
DR HSSP; Q45560; 1BWE.
DR InterPro; IPR001450; 4Fe4s_ferredoxin.
DR InterPro; IPR000345; CytC_heme_bind.
DR Pfam; PF00037; fer4_3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 179 AA; 20170 MW; AB6C1E1748FA4653 CRC64;

```

Query Match 47.1%; Score 41; DB 16; Length 179;
 Best Local Similarity 58.3%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RIVQCRSVEGSC 14
 : | : | | | | |
 Db 117 KAVECRSCDSC 128

RESULT 36

ID Q9MIL9 PRELIMINARY; PRT; 372 AA.
 AC Q9MIL9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 39.9 KDA PROTEIN.
 GN F18P9_20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
 RA Welchselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
 RA Quetier F., Salanoubat M.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; ALI38654; CAB86673.1; -;
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zfc-CCHC; 4.
 DR SMART; SM00343; Znf_C2HC; 4.
 KW Hypothetical protein; Zinc-finger.
 SQ SEQUENCE 372 AA; 39913 MW; 66E39D42E5E3F1D2 CRC64;

Query Match 47.1%; Score 41; DB 10; Length 372;
 Best Local Similarity 63.6%; Pred. No. 24;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 QCRSVEGSCGF 16
 : | : | | | | |
 Db 189 RCPVFGSCGF 199

RESULT 37

ID Q62390 PRELIMINARY; PRT; 554 AA.
 AC Q62390;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE INT-3 PROTEIN.
 GN NOTCH4 OR INT-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RA TISSUE-LUNG, AND TESTIS;
 RC MEDLINE=96281668; PubMed=8681805;
 RX Uytendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
 RA "Notch4/Int-3, a mammary proto-oncogene, is an endothelial cell-
 RT specific mammalian Notch gene.";
 RL Development 122:2251-2259(1996).
 DR EMBL; U43691; AAC52631.1; -;

DR HSSP; P25963; IIKN.
 DR MGD; MGI:107471; Notch4.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 6.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 5.
 DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 554 AA; 58351 MW; 5E59375C5353BC0F CRC64;

Query Match 47.1%; Score 41; DB 11; Length 554;
 Best Local Similarity 70.0%; Pred. No. 35;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 QCRSVEGSCG 15
 : | | | | | | |
 Db 465 RCRSRGSCG 474

RESULT 38

QY784
 ID Q9Y784 PRELIMINARY; PRT; 631 AA.
 AC Q9Y784;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE INTEGRAL MEMBRANE PROTEIN.
 GN PTH1.
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthae.
 OX NCBI_TaxID=148305;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=4091-5-8;
 RX MEDLINE=99452735; PubMed=10521529;
 RA DeZwaan T.M., Carroll A.M., Valent B., Sweigard J.A.;
 RT "Magnaporthe grisea Pth1p is a novel plasma membrane protein that
 RT mediates appressorium differentiation in response to inductive
 RT substrate cues.";
 RL Plant Cell 11:2013-2030(1999).
 DR EMBL; AF119670; AAD30436.1; -;
 SQ SEQUENCE 631 AA; 69349 MW; B7F377C417635279 CRC64;

Query Match 47.1%; Score 41; DB 3; Length 631;
 Best Local Similarity 47.6%; Pred. No. 40;
 Matches 10; Conservative 1; Mismatches 2; Indels 8; Gaps 1;

QY 2 LRIVQC-----RSVEGSC 14
 | | | | |
 Db 240 LVIVQCLPVAAYDRSIEGKC 260

RESULT 39

ID Q9NF74 PRELIMINARY; PRT; 707 AA.
 AC Q9NF74;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE EG:BACR7A4.15 PROTEIN.
 GN EG:BACR7A4.15 OR CG3703.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Papagiannakis G., Spanos L., Bolshakov V., Siden-Kiamos I., Louis C.;

RT Sequencing the distal X chromosome of Drosophila melanogaster.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA Benos P.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL109630; CAB51686.1;
DR FlyBase: FBgn040348; EG: BACR7A4.15.
DR InterPro: IPR004012; Run.
DR Pfam: PF02759; RUN; 1.
SQ SEQUENCE 711 AA; 78093 MW; 5D78E6A8E2432B06 CRC64;

Query Match 47.1%; Score 41; DB 5; Length 707;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 YLRIVQCRSVEGSCG 15
:: :||:|||||
DB 266 FIAFLQCDIAEGSVG 280

RESULT 40

ID Q9W5C1 PRELIMINARY; PRT; 711 AA.
AC Q9W5C1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE CG3703 PROTEIN.
GN EG: BACR7A4.15 OR CG3703.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pohlard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
DR EMBL: AE003419; AAF45572.1;
DR FlyBase: FBgn040348; EG: BACR7A4.15.
DR InterPro: IPR004012; Run.
DR Pfam: PF02759; RUN; 1.
SQ SEQUENCE 711 AA; 78612 MW; B8547DA2ABA1779F CRC64;

Query Match 47.1%; Score 41; DB 5; Length 711;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 YLRIVQCRSVEGSCG 15
:: :||:|||||
DB 270 FIAFLQCDIAEGSVG 284

RESULT 41

ID O35442 PRELIMINARY; PRT; 1964 AA.
AC O35442;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NOTCH4.
GN NOTCH4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.,
RT "Sequence of the mouse major histocompatibility locus class III
region.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030001; AAB82004.1;
DR HSSP: P08709; 1BF9.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR000800; Notch.
DR InterPro: IPR001281; Rieske.
DR Pfam: PF00023; ank; 6.
DR Pfam: PF00008; EGF; 27.
DR Pfam: PF00066; notch; 2.
DR PRINTS: PR01415; ANKYRIN.
DR PRINTS: PR00010; EGFBLD.
DR PRINTS: PR01452; NOTCH.
DR SMART: SM00248; ANK; 5.
DR SMART: SM00179; EGF_Ca; 12.
DR SMART: SM00001; EGF_like; 14.
DR SMART: SM00004; NL; 2.
DR PROSITE: PS50088; ANK_REPEAT; 5.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 11.
DR PROSITE: PS00022; EGF_1; UNKNOWN_28.
DR PROSITE: PS01186; EGF_2; 21.
DR PROSITE: PS01187; EGF_Ca; 9.
DR PROSITE: PS00200; RIESKE_2; UNKNOWN_1.
KW ANK repeat; Calcium-binding; EGF-like domain; Glycoprotein;
KW Hydroxylation; Repeat
SQ SEQUENCE 1964 AA; 206700 MW; 53D7F86394FC40BD CRC64;

Query Match 47.1%; Score 41; DB 11; Length 1964;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 QCRSVEGSCG 15
 :||| ||||
 Db 1875 KCRSRGSCG 1884

RESULT 42

ID O46625 PRELIMINARY; PRT; 134 AA.
 AC O46625;
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BTRAPPIN-2 PROTEIN (FRAGMENT).
 GN BTRAPPIN-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RA Zeeuwen P.L.J.M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RX MEDLINE=97400522; PubMed=9252357;
 RA Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;
 RT Identification and Sequence Analysis of Two New Members of the
 RT SKALP/elafin and SPAL-2 Gene Family; Biochemical Properties of the
 RT Transglutaminase Substrate Motif and Suggestions for a New
 RT Nomenclature.;
 RL J. Biol. Chem. 272:20471-20478(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RX MEDLINE=93280175; PubMed=7685029;
 RA Molhuizen H.O., Alkemade H.A., Zeeuwen P.L., de Jong G.J.,
 RA Wieringa B., Schalkwijk J.;
 RT SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes
 RT Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-
 RT Linking.;
 RL J. Biol. Chem. 268:12028-12032(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RX MEDLINE=96215132; PubMed=8636131;
 RA Tachibana S., Hirose S.;
 RA "Accelerated evolution in inhibitor domains of porcine elafin family
 RT members";
 RL J. Biol. Chem. 271:7012-7018(1996).
 DR EMBL; AJ223216; CAA11184.1; -
 DR HSSP; P19957; 2REL.
 DR InterPro; IPR000737; Squash.
 DR InterPro; IPR002098; SVP-I.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00003; ADSULPHCORE.
 DR PRODOM; PD001224; WAP; 1.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4_DSULFIDE_CORE; 1.
 DR PROSITE; PS00313; SVP-I; 2.
 FT NON_TER 1
 SQ SEQUENCE 134 AA; 14324 MW; CDC7C13D4228A955 CRC64;

Query Match 46.0%; Score 40; DB 6; Length 134;
 Best Local Similarity 55.6%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 2 LRIVQCRSV-----EGSCG 15
 || || | |||||
 Db 110 LRDAQCPGVKKCEGSCG 127

RESULT 43

ID Q9DJL2 PRELIMINARY; PRT; 167 AA.
 AC Q9DJL2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CRME PROTEIN.
 GN CRME.
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ELEPHANTPOX;
 RX MEDLINE=20569353; PubMed=11119592;
 RA Saraiva M., Alcamí A.;
 RT "CrME, a novel soluble tumour necrosis factor receptor encoded by
 RT Poxviruses";
 RL J. Virol. 75:226-233(2001).
 DR HSSP; P19438; 1EXT.
 DR EMBL; AJ272008; CAC15562.1; -
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR PRODOM; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS00500; TNFR_NGFR_2; 2.
 SQ SEQUENCE 167 AA; 18500 MW; FB790E7927F91680 CRC64;

Query Match 46.0%; Score 40; DB 12; Length 167;
 Best Local Similarity 53.3%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 YLRIVQCRSVEGSCG 15
 || | | | ||||
 Db 70 YNRSPWCHSCGSCG 84

RESULT 44

ID Q9X8T3 PRELIMINARY; PRT; 197 AA.
 AC Q9X8T3;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 20.3 KDA PROTEIN.
 GN SCH24.19C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

```

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL049826; CAB2725.1; -.
KW Hypothetical protein.
SQ SEQUENCE 197 AA; 20317 MW; DCC41852B19B3CFE CRC64;

Query Match 46.0%; Score 40; DB 2; Length 197;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 QCRSVEGSCGF 16
Db 170 ECRKVDGATGF 180

RESULT 45
ID P73692 PRELIMINARY; PRT; 265 AA.
AC P73692;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 29.8 KDA PROTEIN.
GN SLR1809.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyaajima N., Hirotsawa M., Suglura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90908; BAA17739.1; -.
DR InterPro; IPR001440; TPR.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 265 AA; 29760 MW; 3A344CF7BDC25569 CRC64;

Query Match 46.0%; Score 40; DB 16; Length 265;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YLRIVQCRSVEGSC 14
Db 114 HLRVRQCLSLPGC 127

RESULT 46
ID Q9S530 PRELIMINARY; PRT; 354 AA.
AC Q9S530;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UDP-3-O-[3-HYDROXYMYRISTOYL] GLUCOSAMINE N-ACYLTRANSFERASE LPXD.
GN LPXD.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

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OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LGV-434;
RX MEDLINE=99392470; PubMed=10463174;
RA Bannantine J.P., Rokey D.D.;
RT "Use of primate model system to identify Chlamydia trachomatis protein
RT antigens recognized uniquely in the context of infection.";
RL Microbiol. 145:2077-2085(1999).
DR EMBL; AF077009; AAC35947.1; -.
DR InterPro; IPR001451; Hexapep_transf.
DR Pfam; PF00132; hexapep; 8.
KW Transferase; Acyltransferase.
SQ SEQUENCE 354 AA; 38493 MW; 7972D0C013233EF9 CRC64;

Query Match 46.0%; Score 40; DB 2; Length 354;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 IVQCRSVEGSCGF 16
Db 178 IIPGAVIGSCGF 190

RESULT 47
ID O84245 PRELIMINARY; PRT; 354 AA.
AC O84245;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UDP-3-O-[3-HYDROXYMYRISTOYL] GLUCOSAMINE N-ACYLTRANSFERASE.
GN LPXD OR CT243.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UN-3/CX;
RX MEDLINE=99008009; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
DR EMBL; AE001297; AAC67836.1; -.
DR InterPro; IPR001451; Hexapep_transf.
DR Pfam; PF00132; hexapep; 8.
KW Transferase; Acyltransferase; Complete proteome.
SQ SEQUENCE 354 AA; 38404 MW; B9C547C129AE17BB CRC64;

Query Match 46.0%; Score 40; DB 16; Length 354;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 IVQCRSVEGSCGF 16
Db 178 IIPGAVIGSCGF 190

RESULT 48
ID Q928N6 PRELIMINARY; PRT; 360 AA.
AC Q928N6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UDP GLUCOSAMINE N-ACYLTRANSFERASE.
GN LPXD OR CPN0302 OR CP0456.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).

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CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
DR EMBL: AF206500; AAF19840.1; -.
DR InterPro: IPR000970; Wnt1.
DR Pfam: PF00110; wnt; 1.
DR SMART: SM00097; WNT1; 1.
DR PROSITE: PS00246; WNT1; 1.
DR Developmental protein; Glycoprotein.
SQ SEQUENCE 362 AA; 40512 MW; CED903393AD54F23 CRC64;

Query Match 46.0%; Score 40; DB 5; Length 362;
Best Local Similarity 50.0%; Pred.No. 35;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 RIVQCRSVEGSC 14
Db 184 RVCKCHGVGSC 195

RESULT 50
Q9NCP9 PRELIMINARY; PRT; 364 AA.
AC Q9NCP9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE WNT8.
DE GN WNT8.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OC NCBI_TaxID=7739;
[1]
SEQUENCE FROM N.A.
MEDLINE=21155807; PubMed=11258394;
Schubert M., Holland L.Z., Panopoulou G.D., Lehrach H., Holland N.D.;
"Characterization of amphioxus Amphioxus insights into the evolution
of patterning of the embryonic dorsoventral axis.";
Evol. Dev. 2:85-92(2000).
CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
DR EMBL: AF190470; AAF80559.1; -.
DR InterPro: IPR000970; Wnt1.
DR Pfam: PF00110; wnt; 1.
DR PRINTS: PR01349; WNTPROTEIN.
DR SMART: SM00097; WNT1; 1.
DR PROSITE: PS00246; WNT1; 1.
DR Developmental protein; Glycoprotein.
SQ SEQUENCE 364 AA; 40514 MW; 12C105C3CCD45D60 CRC64;

Query Match 46.0%; Score 40; DB 5; Length 364;
Best Local Similarity 50.0%; Pred.No. 35;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 RIVQCRSVEGSC 14
Db 184 RVCKCHGVGSC 195

Search completed: July 10, 2002, 08:28:51
Job time: 208 sec

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